

## **Genomic Sequences of Two Novel *Levivirus* ssRNA Coliphages (Family *Leviviridae*): Evidence for Recombination in Environmental Strains**

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Male-specific ssRNA coliphages (FRNA), family *Leviviridae*, contain two genera, *Levivirus* and *Allolevivirus*, and four distinct genogroups (I, II, III and IV). During an environmental FRNA study two novel strains became evident when nucleotide sequences and phylogenetic analysis of a 189 bp amplicon clustered the strains between *Levivirus* genogroups I and II, leading to a proposed genogroup I *Levivirus* subcluster, termed JS-like. In the present study, numerous strains from genogroups I and II, including two JS strains, were used to examine the genomic and phylogenetic relationships. The two JS strains shared a nucleotide similarity of 96.73% to each other and only an 80-84 % similarity to nine MS2-like genogroup I strains. Amino acid composition between JS strains and MS-2 like strains of the maturation, capsid and lysis proteins shared 99-100%, 98-100% and 95-100%, respectively. However, the replicase amino acid sequences were 84-85% similar. Analysis of complete genome sequences, amino acid composition, phylogenetic relationships and four recombination programs suggests the JS strains are recombinants. These two JS environmental FRNA strains are the first description of a viral recombinant from natural isolates in ssRNA *Leviviridae* bacteriophages.

1085 characters

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